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RAW SEQUENCE LISTING

DATE: 03/26/2002

PATENT APPLICATION: US/09/995,693

TIME: 09:49:05

Input Set : N:\Crf3\RULE60\09995693.raw

Output Set: N:\CRF3\03262002\I995693.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Schwall, Ralph H.

6 Tabor, Kelly H.

8 (ii) TITLE OF INVENTION: Hepatocyte Growth Factor Receptor

9 Antagonists and Uses Thereof

11 (iii) NUMBER OF SEQUENCES: 4

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Genentech, Inc.

15 (B) STREET: 1 DNA Way

16 (C) CITY: South San Francisco

17 (D) STATE: California

18 (E) COUNTRY: USA

19 (F) ZIP: 94080

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: WinPatin (Genentech)

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/995,693

C--> 29 (B) FILING DATE: 29-Nov-2001

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 08/952,235

34 (B) FILING DATE:

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Marschang, Diane L.

38 (B) REGISTRATION NUMBER: 35,600

39 (C) REFERENCE/DOCKET NUMBER: P0938P1

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: 650/225-5416

43 (B) TELEFAX: 650/952-9881

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 220 amino acids

48 (B) TYPE: Amino Acid

49 (D) TOPOLOGY: Linear

51 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

53 Asp Ile Met Met Ser Gln Ser Pro Ser Ser Leu Thr Val Ser Val

54 1 5 10 15

56 Gly Glu Lys Val Thr Val Ser Cys Lys Ser Ser Gln Ser Leu Leu

57 20 25 30

ENTERED

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59 Tyr Thr Ser Ser Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
60                      35                      40                      45
62 Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
63                      50                      55                      60
65 Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
66                      65                      70                      75
68 Asp Phe Thr Leu Thr Ile Thr Ser Val Lys Ala Asp Asp Leu Ala
69                      80                      85                      90
71 Val Tyr Tyr Cys Gln Gln Tyr Tyr Ala Tyr Pro Trp Thr Phe Gly
72                      95                      100                     105
74 Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
75                      110                     115                     120
77 Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
78                      125                     130                     135
80 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
81                      140                     145                     150
83 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
84                      155                     160                     165
86 Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
87                      170                     175                     180
89 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
90                      185                     190                     195
92 Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
93                      200                     205                     210
95 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
96                      215                     220

```

98 (2) INFORMATION FOR SEQ ID NO: 2:

100 (i) SEQUENCE CHARACTERISTICS:

101 (A) LENGTH: 230 amino acids

102 (B) TYPE: Amino Acid

103 (D) TOPOLOGY: Linear

105 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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107 Glx Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly
108 1 5 10 15
110 Ala Ser Val Lys Met Ser Cys Arg Ala Ser Gly Tyr Thr Phe Thr
111 20 25 30
113 Ser Tyr Trp Leu His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
114 35 40 45
116 Glu Trp Ile Gly Met Ile Asp Pro Ser Asn Ser Asp Thr Arg Phe
117 50 55 60
119 Asn Pro Asn Phe Lys Asp Lys Ala Thr Leu Asn Val Asp Arg Ser
120 65 70 75
122 Ser Asn Thr Ala Tyr Met Leu Leu Ser Ser Leu Thr Ser Ala Asp
123 80 85 90
125 Ser Ala Val Tyr Tyr Cys Ala Thr Tyr Gly Ser Tyr Val Ser Pro
126 95 100 105
128 Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
129 110 115 120
131 Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys

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132          125          130          135
134 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
135          140          145          150
137 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
138          155          160          165
140 Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
141          170          175          180
143 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
144          185          190          195
146 Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
147          200          205          210
149 Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
150          215          220          225
152 His Thr Ala Ala Pro
153          230
155 (2) INFORMATION FOR SEQ ID NO: 3:
157   (i) SEQUENCE CHARACTERISTICS:
158       (A) LENGTH: 660 base pairs
159       (B) TYPE: Nucleic Acid
160       (C) STRANDEDNESS: Single
161       (D) TOPOLOGY: Linear
163   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
166   GAC ATT ATG ATG TCC CAG TCT CCA TCC TCC CTA ACT 36
167   Asp Ile Met Met Ser Gln Ser Pro Ser Ser Leu Thr
168       1          5          10
170 GTG TCA GTT GGA GAG AAG GTT ACT GTG AGC TGC AAG TCC 75
171 Val Ser Val Gly Glu Lys Val Thr Val Ser Cys Lys Ser
172       15          20          25
174 AGT CAG TCC CTT TTA TAT ACT AGC AGT CAG AAG AAC TAC 114
175 Ser Gln Ser Leu Leu Tyr Thr Ser Ser Gln Lys Asn Tyr
176       30          35
178 TTG GCC TGG TAC CAG CAG AAA CCA GGT CAG TCT CCT AAA 153
179 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
180       40          45          50
182 CTG CTG ATT TAC TGG GCA TCC ACT AGG GAA TCT GGG GTC 192
183 Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
184       55          60
186 CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC 231
187 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
188       65          70          75
190 ACT CTC ACC ATC ACC AGT GTG AAG GCT GAC GAC CTG GCA 270
191 Thr Leu Thr Ile Thr Ser Val Lys Ala Asp Asp Leu Ala
192       80          85          90
194 GTT TAT TAC TGT CAG CAA TAT TAT GCC TAT CCG TGG ACG 309
195 Val Tyr Tyr Cys Gln Gln Tyr Tyr Ala Tyr Pro Trp Thr
196       95          100
198 TTC GGT GGA GGC ACA AAG TTG GAG ATC AAA CGG ACC GTG 348
199 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
200      105          110          115

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202 GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG 387
203 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
204          120          125
206 CAG TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG CTG 426
207 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
208 130          135          140
210 AAT AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG 465
211 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
212          145          150          155
214 GTG GAT AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT 504
215 Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
216          160          165
218 GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC AGC CTC 543
219 Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
220 170          175          180
222 AGC AGC ACC CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA 582
223 Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
224          185          190
226 CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT CAG GGC CTG 621
227 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
228 195          200          205
230 AGC TCG CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT 660
231 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
232 210          215          220
234 (2) INFORMATION FOR SEQ ID NO: 4:
236 (i) SEQUENCE CHARACTERISTICS:
237 (A) LENGTH: 690 base pairs
238 (B) TYPE: Nucleic Acid
239 (C) STRANDEDNESS: Single
240 (D) TOPOLOGY: Linear
242 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
245 SAG GTT CAG CTG CAG CAG TCT GGG CCT GAA CTG GTG 36
246 Glx Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val
247 1          5          10
249 AGG CCT GGG GCT TCA GTG AAA ATG TCC TGC AGG GCT TCG 75
250 Arg Pro Gly Ala Ser Val Lys Met Ser Cys Arg Ala Ser
251 15          20          25
253 GGC TAT ACC TTC ACC AGC TAC TGG TTG CAC TGG GTT AAA 114
254 Gly Tyr Thr Phe Thr Ser Tyr Trp Leu His Trp Val Lys
255 30          35
257 CAG AGG CCT GGA CAA GGC CTT GAG TGG ATT GGC ATG ATT 153
258 Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Met Ile
259 40          45          50
261 GAT CCT TCC AAT AGT GAC ACT AGG TTT AAT CCG AAC TTC 192
262 Asp Pro Ser Asn Ser Asp Thr Arg Phe Asn Pro Asn Phe
263 55          60
265 AAG GAC AAG GCC ACA TTG AAT GTA GAC AGA TCT TCC AAC 231
266 Lys Asp Lys Ala Thr Leu Asn Val Asp Arg Ser Ser Asn
267 65          70          75

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269 ACA GCC TAC ATG CTG CTC AGC AGC CTG ACA TCT GCT GAC 270
270 Thr Ala Tyr Met Leu Leu Ser Ser Leu Thr Ser Ala Asp
271      80                      85                      90
273 TCT GCA GTC TAT TAC TGT GCC ACA TAT GGT AGC TAC GTT 309
274 Ser Ala Val Tyr Tyr Cys Ala Thr Tyr Gly Ser Tyr Val
275      95                      100
277 TCC CCT CTG GAC TAC TGG GGT CAA GGA ACC TCA GTC ACC 348
278 Ser Pro Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
279     105                      110                      115
281 GTC TCT TCC GCC TCC ACC AAG GGC CCA TCG GTC TTC CCC 387
282 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
283      120                      125
285 CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG 426
286 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
287     130                      135                      140
289 GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG 465
290 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
291     145                      150                      155
293 GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC 504
294 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
295     160                      165
297 GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC 543
298 Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
299     170                      175                      180
301 TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC 582
302 Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
303     185                      190
305 TTG GGC ACC CAG ACC TAC ATC TGC AAC GTG AAT CAC AAG 621
306 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
307     195                      200                      205
309 CCC AGC AAC ACC AAG GTC GAC AAG AAA GTT GAG CCC AAA 660
310 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
311     210                      215                      220
313 TCT TGT GAC AAA ACT CAC ACA GCT GCG CCG 690
314 Ser Cys Asp Lys Thr His Thr Ala Ala Pro
315      225                      230

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VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]